

SEQUENCE LISTING

<110> Daiichi Suntory Pharma Co., Ltd.  
 <120> Method for expansion of pluripotent stem cells  
 <130> DSTY-R678/PCT (fP05-02WO-1)  
 <160> 24  
 <170> PatentIn version 3.1  
 <210> 1  
 <211> 882  
 <212> PRT  
 <213> Human E-cadherin

<220>  
 <221> DOMAIN  
 <222> (157) .. (262)  
 <223> EC1

<220>  
 <221> DOMAIN  
 <222> (265) .. (375)  
 <223> EC2

<220>  
 <221> DOMAIN  
 <222> (378) .. (486)  
 <223> EC3

<220>  
 <221> DOMAIN  
 <222> (487) .. (595)  
 <223> EC4

<220>  
 <221> DOMAIN  
 <222> (596) .. (700)  
 <223> EC5

<400> 1

Met	Gly	Pro	Trp	Ser	Arg	Ser	Leu	Ser	Ala	Leu	Leu	Leu	Leu	Gln
1				5				10					15	

Val	Ser	Ser	Trp	Leu	Cys	Gln	Glu	Pro	Glu	Pro	Cys	His	Pro	Gly	Phe
				20				25					30		

Asp Ala Glu Ser Tyr Thr Phe Thr Val Pro Arg Arg His Leu Glu Arg  
 35 40 45

Gly Arg Val Leu Gly Arg Val Asn Phe Glu Asp Cys Thr Gly Arg Gln  
 50 55 60

Arg Thr Ala Tyr Phe Ser Leu Asp Thr Arg Phe Lys Val Gly Thr Asp  
 65 70 75 80

Gly Val Ile Thr Val Lys Arg Pro Leu Arg Phe His Asn Pro Gln Ile  
 85 90 95

His Phe Leu Val Tyr Ala Trp Asp Ser Thr Tyr Arg Lys Phe Ser Thr  
 100 105 110

Lys Val Thr Leu Asn Thr Val Gly His His His Arg Pro Pro Pro His  
 115 120 125

Gln Ala Ser Val Ser Gly Ile Gln Ala Glu Leu Leu Thr Phe Pro Asn  
 130 135 140

Ser Ser Pro Gly Leu Arg Arg Gln Lys Arg Asp Trp Val Ile Pro Pro  
 145 150 155 160

Ile Ser Cys Pro Glu Asn Glu Lys Gly Pro Phe Pro Lys Asn Leu Val  
 165 170 175

Gln Ile Lys Ser Asn Lys Asp Lys Glu Gly Lys Val Phe Tyr Ser Ile  
 180 185 190

Thr Gly Gln Gly Ala Asp Thr Pro Pro Val Gly Val Phe Ile Ile Glu  
 195 200 205

Arg Glu Thr Gly Trp Leu Lys Val Thr Glu Pro Leu Asp Arg Glu Arg  
 210 215 220

Ile Ala Thr Tyr Thr Leu Phe Ser His Ala Val Ser Ser Asn Gly Asn  
 225 230 235 240

Ala Val Glu Asp Pro Met Glu Ile Leu Ile Thr Val Thr Asp Gln Asn  
 245 250 255

Asp Asn Lys Pro Glu Phe Thr Gln Glu Val Phe Lys Gly Ser Val Met

260	265	270
Glu Gly Ala Leu Pro Gly Thr	Ser Val Met Glu Val Thr	Ala Thr Asp
275	280	285
Ala Asp Asp Asp Val Asn Thr Tyr	Asn Ala Ala Ile Ala Tyr Thr	Ile
290	295	300
Leu Ser Gln Asp Pro Glu Leu Pro Asp Lys	Asn Met Phe Thr Ile Asn	
305	310	315
Arg Asn Thr Gly Val Ile Ser Val Val Thr Thr Gly Leu Asp Arg Glu		
325	330	335
Ser Phe Pro Thr Tyr Thr Leu Val Val Gln Ala Ala Asp Leu Gln Gly		
340	345	350
Glu Gly Leu Ser Thr Thr Ala Thr Ala Val Ile Thr Val Thr Asp Thr		
355	360	365
Asn Asp Asn Pro Pro Ile Phe Asn Pro Thr Thr Tyr Lys Gly Gln Val		
370	375	380
Pro Glu Asn Glu Ala Asn Val Val Ile Thr Thr Leu Lys Val Thr Asp		
385	390	395
Ala Asp Ala Pro Asn Thr Pro Ala Trp Glu Ala Val Tyr Thr Ile Leu		
405	410	415
Asn Asp Asp Gly Gly Gln Phe Val Val Thr Thr Asn Pro Val Asn Asn		
420	425	430
Asp Gly Ile Leu Lys Thr Ala Lys Gly Leu Asp Phe Glu Ala Lys Gln		
435	440	445
Gln Tyr Ile Leu His Val Ala Val Thr Asn Val Val Pro Phe Glu Val		
450	455	460
Ser Leu Thr Thr Ser Thr Ala Thr Val Thr Val Asp Val Leu Asp Val		
465	470	475
Asn Glu Ala Pro Ile Phe Val Pro Pro Glu Lys Arg Val Glu Val Ser		
485	490	495

Glu Asp Phe Gly Val Gly Gln Glu Ile Thr Ser Tyr Thr Ala Gln Glu  
500 505 510

Pro Asp Thr Phe Met Glu Gln Lys Ile Thr Tyr Arg Ile Trp Arg Asp  
515 520 525

Thr Ala Asn Trp Leu Glu Ile Asn Pro Asp Thr Gly Ala Ile Ser Thr  
530 535 540

Arg Ala Glu Leu Asp Arg Glu Asp Phe Glu His Val Lys Asn Ser Thr  
545 550 555 560

Tyr Thr Ala Leu Ile Ile Ala Thr Asp Asn Gly Ser Pro Val Ala Thr  
565 570 575

Gly Thr Gly Thr Leu Leu Leu Ile Leu Ser Asp Val Asn Asp Asn Ala  
580 585 590

Pro Ile Pro Glu Pro Arg Thr Ile Phe Phe Cys Glu Arg Asn Pro Lys  
595 600 605

Pro Gln Val Ile Asn Ile Ile Asp Ala Asp Leu Pro Pro Asn Thr Ser  
610 615 620

Pro Phe Thr Ala Glu Leu Thr His Gly Ala Ser Ala Asn Trp Thr Ile  
625 630 635 640

Gln Tyr Asn Asp Pro Thr Gln Glu Ser Ile Ile Leu Lys Pro Lys Met  
645 650 655

Ala Leu Glu Val Gly Asp Tyr Lys Ile Asn Leu Lys Leu Met Asp Asn  
660 665 670

Gln Asn Lys Asp Gln Val Thr Thr Leu Glu Val Ser Val Cys Asp Cys  
675 680 685

Glu Gly Ala Ala Gly Val Cys Arg Lys Ala Gln Pro Val Glu Ala Gly  
690 695 700

Leu Gln Ile Pro Ala Ile Leu Gly Ile Leu Gly Gly Ile Leu Ala Leu  
705 710 715 720

Leu Ile Leu Ile Leu Leu Leu Leu Leu Phe Leu Arg Arg Arg Ala Val  
725 730 735

Val Lys Glu Pro Leu Leu Pro Pro Glu Asp Asp Thr Arg Asp Asn Val  
740 745 750

Tyr Tyr Tyr Asp Glu Glu Gly Gly Gly Glu Glu Asp Gln Asp Phe Asp  
755 760 765

Leu Ser Gln Leu His Arg Gly Leu Asp Ala Arg Pro Glu Val Thr Arg  
770 775 780

Asn Asp Val Ala Pro Thr Leu Met Ser Val Pro Arg Tyr Leu Pro Arg  
785 790 795 800

Pro Ala Asn Pro Asp Glu Ile Gly Asn Phe Ile Asp Glu Asn Leu Lys  
805 810 815

Ala Ala Asp Thr Asp Pro Thr Ala Pro Pro Tyr Asp Ser Leu Leu Val  
820 825 830

Phe Asp Tyr Glu Gly Ser Gly Ser Glu Ala Ala Ser Leu Ser Ser Leu  
835 840 845

Asn Ser Ser Glu Ser Asp Lys Asp Gln Asp Tyr Asp Tyr Leu Asn Glu  
850 855 860

Trp Gly Asn Arg Phe Lys Lys Leu Ala Asp Met Tyr Gly Gly Gly Glu  
865 870 875 880

Asp Asp

<210> 2  
<211> 884  
<212> PRT  
<213> Mouse E-cadherin

<220>  
<221> DOMAIN  
<222> (159) .. (264)  
<223> EC1

<220>

<221> DOMAIN  
 <222> (267) .. (377)  
 <223> EC2

<220>  
 <221> DOMAIN  
 <222> (380) .. (488)  
 <223> EC3

<220>  
 <221> DOMAIN  
 <222> (489) .. (597)  
 <223> EC4

<220>  
 <221> DOMAIN  
 <222> (598) .. (702)  
 <223> EC5

<400> 2

Met Gly Ala Arg Cys Arg Ser Phe Ser Ala Leu Leu Leu Leu Leu Gln  
 1 5 10 15

Val Ser Ser Trp Leu Cys Gln Glu Leu Glu Pro Glu Ser Cys Ser Pro  
 20 25 30

Gly Phe Ser Ser Glu Val Tyr Thr Phe Pro Val Pro Glu Arg His Leu  
 35 40 45

Glu Arg Gly His Val Leu Gly Arg Val Arg Phe Glu Gly Cys Thr Gly  
 50 55 60

Arg Pro Arg Thr Ala Phe Phe Ser Glu Asp Ser Arg Phe Lys Val Ala  
 65 70 75 80

Thr Asp Gly Thr Ile Thr Val Lys Arg His Leu Lys Leu His Lys Leu  
 85 90 95

Glu Thr Ser Phe Leu Val Arg Ala Arg Asp Ser Ser His Arg Glu Leu  
 100 105 110

Ser Thr Lys Val Thr Leu Lys Ser Met Gly His His His His Arg His  
 115 120 125

His His Arg Asp Pro Ala Ser Glu Ser Asn Pro Glu Leu Leu Met Phe  
 130 135 140

Pro Ser Val Tyr Pro Gly Leu Arg Arg Gln Lys Arg Asp Trp Val Ile  
 145 150 155 160

Pro Pro Ile Ser Cys Pro Glu Asn Glu Lys Gly Glu Phe Pro Lys Asn  
 165 170 175

Leu Val Gln Ile Lys Ser Asn Arg Asp Lys Glu Thr Lys Val Phe Tyr  
 180 185 190

Ser Ile Thr Gly Gln Gly Ala Asp Lys Pro Pro Val Gly Val Phe Ile  
 195 200 205

Ile Glu Arg Glu Thr Gly Trp Leu Lys Val Thr Gln Pro Leu Asp Arg  
 210 215 220

Glu Ala Ile Ala Lys Tyr Ile Leu Tyr Ser His Ala Val Ser Ser Asn  
 225 230 235 240

Gly Glu Ala Val Glu Asp Pro Met Glu Ile Val Ile Thr Val Thr Asp  
 245 250 255

Gln Asn Asp Asn Arg Pro Glu Phe Thr Gln Pro Val Phe Glu Gly Phe  
 260 265 270

Val Ala Glu Gly Ala Val Pro Gly Thr Ser Val Met Lys Val Ser Ala  
 275 280 285

Thr Asp Ala Asp Asp Asp Val Asn Thr Tyr Asn Ala Ala Ile Ala Tyr  
 290 295 300

Thr Ile Val Ser Gln Asp Pro Glu Leu Pro His Lys Asn Met Phe Thr  
 305 310 315 320

Val Asn Arg Asp Thr Gly Val Ile Ser Val Leu Thr Ser Gly Leu Asp  
 325 330 335

Arg Glu Ser Tyr Pro Thr Tyr Thr Leu Val Val Gln Ala Ala Asp Leu  
 340 345 350

Gln Gly Glu Gly Leu Ser Thr Thr Ala Lys Ala Val Ile Thr Val Lys

355		360		365
Asp Ile Asn Asp Asn Ala Pro Val Phe Asn Pro Ser Thr Tyr Gln Gly				
370		375		380
Gln Val Pro Glu Asn Glu Val Asn Ala Arg Ile Ala Thr Leu Lys Val				
385		390		395
				400
Thr Asp Asp Asp Ala Pro Asn Thr Pro Ala Trp Lys Ala Val Tyr Thr				
	405		410	415
Val Val Asn Asp Pro Asp Gln Gln Phe Val Val Val Thr Asp Pro Thr				
	420		425	430
Thr Asn Asp Gly Ile Leu Lys Thr Ala Lys Gly Leu Asp Phe Glu Ala				
	435		440	445
Lys Gln Gln Tyr Ile Leu His Val Arg Val Glu Asn Glu Glu Pro Phe				
	450		455	460
Glu Gly Ser Leu Val Pro Ser Thr Ala Thr Val Thr Val Asp Val Val				
	465		470	475
				480
Asp Val Asn Glu Ala Pro Ile Phe Met Pro Ala Glu Arg Arg Val Glu				
	485		490	495
Val Pro Glu Asp Phe Gly Val Gly Gln Glu Ile Thr Ser Tyr Thr Ala				
	500		505	510
Arg Glu Pro Asp Thr Phe Met Asp Gln Lys Ile Thr Tyr Arg Ile Trp				
	515		520	525
Arg Asp Thr Ala Asn Trp Leu Glu Ile Asn Pro Glu Thr Gly Ala Ile				
	530		535	540
Phe Thr Arg Ala Glu Met Asp Arg Glu Asp Ala Glu His Val Lys Asn				
	545		550	555
				560
Ser Thr Tyr Val Ala Leu Ile Ile Ala Thr Asp Asp Gly Ser Pro Ile				
	565		570	575
Ala Thr Gly Thr Gly Thr Leu Leu Leu Val Leu Leu Asp Val Asn Asp				
	580		585	590



Asn Ala Pro Ile Pro Glu Pro Arg Asn Met Gln Phe Cys Gln Arg Asn  
595 600 605

Pro Gln Pro His Ile Ile Thr Ile Leu Asp Pro Asp Leu Pro Pro Asn  
610 615 620

Thr Ser Pro Phe Thr Ala Glu Leu Thr His Gly Ala Ser Val Asn Trp  
625 630 635 640

Thr Ile Glu Tyr Asn Asp Ala Ala Gln Glu Ser Leu Ile Leu Gln Pro  
645 650 655

Arg Lys Asp Leu Glu Ile Gly Glu Tyr Lys Ile His Leu Lys Leu Ala  
660 665 670

Asp Asn Gln Asn Lys Asp Gln Val Thr Thr Leu Asp Val His Val Cys  
675 680 685

Asp Cys Glu Gly Thr Val Asn Asn Cys Met Lys Ala Gly Ile Val Ala  
690 695 700

Ala Gly Leu Gln Val Pro Ala Ile Leu Gly Ile Leu Gly Gly Ile Leu  
705 710 715 720

Ala Leu Leu Ile Leu Ile Leu Leu Leu Leu Phe Leu Arg Arg Arg  
725 730 735

Thr Val Val Lys Glu Pro Leu Leu Pro Pro Asp Asp Asp Thr Arg Asp  
740 745 750

Asn Val Tyr Tyr Tyr Asp Glu Glu Gly Gly Gly Glu Glu Asp Gln Asp  
755 760 765

Phe Asp Leu Ser Gln Leu His Arg Gly Leu Asp Ala Arg Pro Glu Val  
770 775 780

Thr Arg Asn Asp Val Ala Pro Thr Leu Met Ser Val Pro Gln Tyr Arg  
785 790 795 800

Pro Arg Pro Ala Asn Pro Asp Glu Ile Gly Asn Phe Ile Asp Glu Asn  
805 810 815

Leu Lys Ala Ala Asp Ser Asp Pro Thr Ala Pro Pro Tyr Asp Ser Leu  
820 825 830

Leu Val Phe Asp Tyr Glu Gly Ser Gly Ser Glu Ala Ala Ser Leu Ser  
835 840 845

Ser Leu Asn Ser Ser Glu Ser Asp Gln Asp Gln Asp Tyr Asp Tyr Leu  
850 855 860

Asn Glu Trp Gly Asn Arg Phe Lys Lys Leu Ala Asp Met Tyr Gly Gly  
865 870 875 880

Gly Glu Asp Asp

<210> 3  
<211> 21  
<212> DNA  
<213> Oct-3/4,size 528 bp,5'primer

<400> 3  
gaagttggag aaggtggaac c 21

<210> 4  
<211> 21  
<212> DNA  
<213> Oct-3/4,size 528 bp,3'primer

<400> 4  
gcctcataact cttctcgttg g 21

<210> 5  
<211> 20  
<212> DNA  
<213> Rex1,size 930 bp,5'primer

<400> 5  
aaagtgagat tagccccgag 20

<210> 6  
<211> 20  
<212> DNA  
<213> Rex1,size 930 bp,3'primer

<400> 6  
tcccatcccc ttcaatagca 20

<210> 7  
 <211> 20  
 <212> DNA  
 <213> Nanog, size 930 bp, 5'primer  
  
 <400> 7  
 gaggaagcat cgaattctgg 20  
  
 <210> 8  
 <211> 20  
 <212> DNA  
 <213> Nanog, size 930 bp, 3'primer  
  
 <400> 8  
 aagttatgga gcggagcagc 20  
  
 <210> 9  
 <211> 19  
 <212> DNA  
 <213> GAPDH, size 858 bp, 5'primer  
  
 <400> 9  
 ggaagcttgt catcaacgg 19  
  
 <210> 10  
 <211> 20  
 <212> DNA  
 <213> GAPDH, size 858 bp, 3'primer  
  
 <400> 10  
 ctcttgctca gtgtccttgc 20  
  
 <210> 11  
 <211> 19  
 <212> DNA  
 <213> NeuroD3, size 405 bp, 5'primer  
  
 <400> 11  
 catctctgat ctcgactgc 19  
  
 <210> 12  
 <211> 19  
 <212> DNA  
 <213> NeuroD3, size 405 bp, 3'primer  
  
 <400> 12  
 ccagatgtag ttgtaggcg 19  
  
 <210> 13  
 <211> 19  
 <212> DNA  
 <213> Sox1, size 407 bp, 5'primer

<400> 13	
gcacacagcg ttttctcgg	19
<210> 14	
<211> 19	
<212> DNA	
<213> Sox1, size 407 bp, 3'primer	
<400> 14	
acatccgact cctcttccc	19
<210> 15	
<211> 20	
<212> DNA	
<213> T/Brachyury, size 528 bp, 5'primer	
<400> 15	
tccaggtgct atatattgcc	20
<210> 16	
<211> 20	
<212> DNA	
<213> T/Brachyury, size 528 bp, 3'primer	
<400> 16	
tgctgcctgt gagtcacaac	20
<210> 17	
<211> 22	
<212> DNA	
<213> Flk1, size 398 bp, 5'primer	
<400> 17	
taggtgcctc cccataccct gg	22
<210> 18	
<211> 22	
<212> DNA	
<213> Flk1, size 398 bp, 3'primer	
<400> 18	
tggccggctc tttcgcttac tg	22
<210> 19	
<211> 19	
<212> DNA	
<213> beta-H1, size 415 bp, 5'primer	
<400> 19	
aaccctcaat ggctgtgg	19

<210>	20	
<211>	22	
<212>	DNA	
<213>	beta-H1, size 415 bp,3'primer	
<400>	20	
	tcagtgggtac ttgtgggaca gc	22
<210>	21	
<211>	20	
<212>	DNA	
<213>	alpha-fetoprotein, size 997 bp,5'primer	
<400>	21	
	tgctcagtac gacaaggctcg	20
<210>	22	
<211>	20	
<212>	DNA	
<213>	alpha-fetoprotein, size 997 bp, 3'primer	
<400>	22	
	actggatgatg catagcctcc	20
<210>	23	
<211>	20	
<212>	DNA	
<213>	transthyretin, size 440 bp, 5'primer	
<400>	23	
	agtcctggat gctgtccgag	20
<210>	24	
<211>	21	
<212>	DNA	
<213>	transthyretin, size 440 bp, 3'primer	
<400>	24	
	tcagaggtcg ggcagcccag c	21